CLUSTAL W (1.82) Multiple Sequence Alignments

```
SEQ ID NO:2:      2_HuPS1          467 aa
SEQ ID NO:134:    134_HuPS1        467 aa
SEQ ID NO:4:      4_MuPS1          461 aa


Sequences (2:134)       Aligned. Score:   99
Sequences (2:4)         Aligned. Score:   89
Sequences (134:4)       Aligned. Score:   89
```

```
2_HuPS1          MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
134_HuPS1        MTELPAPLSYFQNAQMSEDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRPQGNSR 60
4_MuPS1          MTEIPAPLSYFQNAQMSEDSHSSSAIRSQNDSQERQQQHDRQRLDNPEPISNGRPQSNSR 60
                 ***:***************.* *.::*****.:***:::**: *.:***:****** .***


2_HuPS1          QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
134_HuPS1        QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
4_MuPS1          QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE 120
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2_HuPS1          DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
134_HuPS1        DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
4_MuPS1          DTETVGQRALHSILNAAIMISVIVIMTILLVVLYKYRCYKVIHAWLIISSLLLLFFFSFI 180
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2_HuPS1          YLGEVFKTYNVAVDYITVALLIWNLGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
134_HuPS1        YLGEVFKTYNVAVDYITVALLIWNFGVVGMISIHWKGPLRLQQAYLIMISALMALVFIKY 240
4_MuPS1          YLGEVFKTYNV-VDYVTVALLIWNWGVVGMIAIHWKGPLRLQQAYLIMISALMALVFIKY 239
                 ********** ***:******** ******:****************************


2_HuPS1          LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
134_HuPS1        LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 300
4_MuPS1          LPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAE 299
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2_HuPS1          GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
134_HuPS1        GDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSEEWEAQRDSHLGPHRSTPESRAA 360
4_MuPS1          GDPEAQRRVPKNPKYNTQRAERETQDSGSGNDDGGFSEEWEAQRDSHLGPHRSTPESRAA 359
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2_HuPS1          VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
134_HuPS1        VQELSSSILAGEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCL 420
4_MuPS1          VQELSGSILTSEDPEERGVKLGLGDFIFYSVLVGKASATASGDWNTTIAC-VAILIGLCL 418
                 *****.***:.*******************************************  *********


2_HuPS1          TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
134_HuPS1        TLLLLAIFKKALPALPISITFGLVFYFATDYLVQPFMDQLAFHQFYI 467
4_MuPS1          -LLLLAIYKKGP--APISITFGFVF-FATDYLVQPFMDQLAFHQFYI 461
                 ******:**.    ******:** *******************
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